

3/6 #6



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,405

DATE: 03/06/2002 P.5
TIME: 13:01:01

Input Set : A:\SEQ FOR DISK

Output Set: N:\CRF3\03062002\J003405.raw

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3 <110> APPLICANT: Ruan, Yong-Ling
4      Furbank, Robert T.
5      Danny, Llewellyn J.
7 <120> TITLE OF INVENTION: Modification of sucrose synthase gene expression in plant
tissue and
8      uses therefor
10 <130> FILE REFERENCE: GHSUSY W01
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/003,405
C--> 12 <141> CURRENT FILING DATE: 2000-12-18
12 <150> PRIOR APPLICATION NUMBER: 60/251852
13 <151> PRIOR FILING DATE: 2000-12-08
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2625
21 <212> TYPE: DNA
22 <213> ORGANISM: Gossypium hirsutum
24 <220> FEATURE:
25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (1240)..(1240)
27 <223> OTHER INFORMATION: n = any nucleotide (a,g,c,t)
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(2625)
32 <223> OTHER INFORMATION:
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36 Met Ala Glu Arg Ala Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu
37 1          5          10          15
39 gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca      96
40 Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser
41          20          25          30
43 agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att      144
44 Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
45          35          40          45
47 cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat      192
48 Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
49          50          55          60
51 ggt gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg      240
52 Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
53 65          70          75          80
55 cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag      288
56 Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
57          85          90          95

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59 tac att aga gtg aat gtt cac gcc ctt gtt gtt gag gaa ctc act gtt      336
60 Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
61          100          105          110
63 gct gag tat ctc cac ttc aag gaa gag ctt gtt gat gga agt tca aat      384
64 Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
65          115          120          125
67 gga aac ttt gtt ttg gaa ttg gat ttt gag ccc ttc aac tca tca ttc      432
68 Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
69          130          135          140
71 ccc cgc cca act ctt tca aaa tcc att ggt aat ggt gtg gag ttc cta      480
72 Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
73 145          150          155          160
75 aat cgt cac ctt tcg gca aaa ttg ttc cat gac aag gag agc atg cac      528
76 Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
77          165          170          175
79 cct ttg ctc gaa ttc ctc aga gtc cat tgt cac aag ggc aag aac atg      576
80 Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
81          180          185          190
83 atg ttg aat gac aga att cag aac ttg aat gct ctt caa cat gtt ttg      624
84 Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
85          195          200          205
87 agg aaa gca gag gag tat ctt ggt acc cta cct cct gag aca cca tgt      672
88 Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
89          210          215          220
91 gcc gaa ttc gaa cac cgg ttc cag gaa atc ggt ttg gaa aga ggt tgg      720
92 Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
93 225          230          235          240
95 ggt gac acc gca gaa cgc gtg ctc gag atg atc caa ctc ctt ttg gat      768
96 Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
97          245          250          255
99 ctt ctt gag gca act gat cct tgc acc ctt gag aag ttc ctt ggg aga      816
100 Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg
101          260          265          270
103 atc ccc atg gtg ttc aat gtt gtg att ctc act ccc cac gga tac ttc      864
104 Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
105          275          280          285
107 gct caa gac aat gtt ttg ggg tat ccc gac acc ggt ggg cag gtt gtt      912
108 Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
109          290          295          300
111 tac atc ttg gat caa gtc cga gct ttg gag aat gag atg ctc ctc cgt      960
112 Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg
113 305          310          315          320
115 ata aag caa caa gga ctc aac atc acc cct cga atc ctc att att act      1008
116 Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr
117          325          330          335
119 aga ctt ctt cct gat gct gtc gga aca aca tgc ggt caa cga ctt gag      1056
120 Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
121          340          345          350
123 aaa gta tac gga aca gag cac tcg gat att ctt cga gta ccc ttc aga      1104

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124 Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg
125          355          360          365
127 aca gaa aag gga att gtt cga aaa tgg atc tca aga ttt gaa aaa gtc 1152
128 Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val
129          370          375          380
131 tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc 1200
132 Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser
133 385          390          395          400
W--> 135 aaa gag ttg cac ggc acg cca gat ctg atc atc gga aac nac agc gac 1248
W--> 136 Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp
137          405          410          415
139 ggc aat atc gtc gcc tcc ttg ctc gca cat aaa tta ggt gtc aca cag 1296
140 Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln
141          420          425          430
143 tgc acc atc gcc cat gct ttg gag aag aca aaa tat cca gat tca gat 1344
144 Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp
145          435          440          445
147 atc tat tgg aag aag ctt gaa gac aaa tac cat ttc tct tgc caa ttt 1392
148 Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe
149          450          455          460
151 aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt 1440
152 Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser
153 465          470          475          480
155 act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag 1488
156 Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu
157          485          490          495
159 agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt 1536
160 Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly
161          500          505          510
163 atc gat gtg ttt gat ccc aaa ttc aac att gtt tcc cct ggt gct gat 1584
164 Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp
165          515          520          525
167 atg gag ata tac ttc cct tac acc gaa gag aag cgg agg ttg aag cat 1632
168 Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His
169          530          535          540
171 ttc cat cct gag atc gaa gac ctt ctt tac acc aaa gtt gag aat gaa 1680
172 Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu
173 545          550          555          560
175 gaa cac tta tgt gtg ctc aat gac cgc aac aag cca att ctg ttc aca 1728
176 Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr
177          565          570          575
179 atg cca agg ctt gat cgt gtc aag aac tta acc gga ctc gtc gag tgg 1776
180 Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp
181          580          585          590
183 tgc ggc aag aac cca aag ttg cgt gag ttg gct aac ctc gta gtt gta 1824
184 Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val
185          595          600          605
187 ggt ggt gat agg cga aag gaa tct aaa gat ttg gaa gag aag gct gaa 1872
188 Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu

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Input Set : A:\SEQ FOR DISK

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189	610	615	620	
191	atg aag aaa atg ttt gag ctg atc gac aag tac aac ttg aac ggc caa	1920		
192	Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln			
193	625 630 635 640			
195	ttc aga tgg ata tca tct caa atg aac aga atc cga aat gtt gaa ctt	1968		
196	Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu			
197	645 650 655			
199	tac cga tac att tgc gac acg aaa ggt gcc ttt gta cag cct gca ttg	2016		
200	Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu			
201	660 665 670			
203	tat gaa gcc ttt gga ttg aca gtt gtg gag gca atg act tgc ggt ttg	2064		
204	Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu			
205	675 680 685			
207	cca aca ttc gca acc tgt aac ggt gga cca gcc gag att att gtc cat	2112		
208	Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His			
209	690 695 700			
211	ggg aaa tct ggt ttc aac att gat cct tac cat ggt gat caa gct gct	2160		
212	Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala			
213	705 710 715 720			
215	gac ata ctc gtc gat ttc ttt gaa aag tgt aag aaa gat cca tct cac	2208		
216	Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His			
217	725 730 735			
219	tgg gat aag atc tcc caa gga ggc ttg aaa cga ata gag gag aag tat	2256		
220	Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr			
221	740 745 750			
223	aca tgg aag att tac tcg gag aga cta ttg acc ctg aca gga gtg tat	2304		
224	Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr			
225	755 760 765			
227	gga ttc tgg aag cat gtt tcc aac ctt gaa cgc cgt gag agt cgt cgt	2352		
228	Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg			
229	770 775 780			
231	tac ctt gag atg ttt tat gct ctt aag tac cgt aag ctg gct gaa tca	2400		
232	Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser			
233	785 790 795 800			
235	gtt cca ttg gca gag gag taa att gaa cct gtt aaa taa cat tgg gcc	2448		
236	Val Pro Leu Ala Glu Glu Ile Glu Pro Val Lys His Trp Ala			
237	805 810			
239	ggt ttt tct tgg aga ata ata ttc tgt ttt gta att tca att gga gaa	2496		
240	Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu			
241	815 820 825 830			
243	gct cct ttg tat ttc atc ttg tct ttt cct ttt cct ttt ttc gcc ggc	2544		
244	Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe Ala Gly			
245	835 840 845			
247	att gtt tga aca tgg ggt tgt gcg ccc gtc aat tcc agt taa ata tgg	2592		
248	Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp			
249	850 855 860			
251	tga ctt ttg ttt ttc aaa aaa aaa aaa aaa aaa	2625		
252	Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys			
253	865 870			

RAW SEQUENCE LISTING

DATE: 03/06/2002

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TIME: 13:01:02

Input Set : A:\SEQ FOR DISK

Output Set: N:\CRF3\03062002\J003405.raw

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255 <210> SEQ ID NO: 2
256 <211> LENGTH: 806
257 <212> TYPE: PRT
258 <213> ORGANISM: Gossypium hirsutum
260 <220> FEATURE:
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: (414)..(414)
263 <223> OTHER INFORMATION: The 'Xaa' at location 414 stands for Asn, Asp, His, or Tyr.
265 <220> FEATURE:
266 <221> NAME/KEY: misc_feature
267 <222> LOCATION: (1240)..(1240)
269 <223> OTHER INFORMATION: n = any nucleotide (a,g,c,t)
271 <400> SEQUENCE: 2
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274 1          5          10          15
276 Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser
277          20          25          30
279 Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
280          35          40          45
282 Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
283          50          55          60
285 Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
286 65          70          75          80
288 Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
289          85          90          95
291 Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
292          100         105         110
294 Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
295          115         120         125
297 Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
298          130         135         140
300 Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
301 145         150         155         160
303 Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
304          165         170         175
306 Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
307          180         185         190
309 Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
310          195         200         205
312 Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
313          210         215         220
316 Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
317 225         230         235         240
319 Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
320          245         250         255
322 Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg
323          260         265         270
325 Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
326          275         280         285

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→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 03/06/2002

PATENT APPLICATION: US/10/003,405

TIME: 13:01:03

Input Set : A:\SEQ FOR DISK

Output Set: N:\CRF3\03062002\J003405.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2